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OIEP

RAW SEQUENCE LISTING

DATE: 06/21/2002

PATENT APPLICATION: US/10/078,531

TIME: 07:18:03

Input Set : A:\Pharma18.app

Output Set: N:\CRF3\06212002\J078531.raw

3 <110> APPLICANT: MARTIN, DENIS
 4 RIOUX, STEPHANE
 5 BRODEUR, BERNARD R.
 6 HAMEL, JOSEE
 7 RHEAULT, PATRICK

9 <120> TITLE OF INVENTION: STREPTOCOCCUS PYOGENES POLYPEPTIDES AND CORRESPONDING
 10 DNA FRAGMENTS

12 <130> FILE REFERENCE: PHARMA-18

14 <140> CURRENT APPLICATION NUMBER: 10/078,531

15 <141> CURRENT FILING DATE: 2002-02-21

17 <150> PRIOR APPLICATION NUMBER: 60/269,840

18 <151> PRIOR FILING DATE: 2001-02-21

20 <160> NUMBER OF SEQ ID NOS: 14

22 <170> SOFTWARE: PatentIn Ver. 2.1

24 <210> SEQ ID NO: 1

25 <211> LENGTH: 3027

26 <212> TYPE: DNA

27 <213> ORGANISM: Streptococcus pyogenes

29 <400> SEQUENCE: 1

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 32 tcgatttctg gcgctgacta cgcagaaagt agcggtaaaa gcaagttaaa gattaatgaa 180
 33 acttctggcc ctggtgatga tacagtcact gacttatttt cggataaacg tactactcct 240
 34 gaaaaaataa aagataatct tgctaaagggt ccgagagaaac aagagttaaa ggcagtaaca 300
 35 gagaatacag aatcagaaaa gcagatcact tctggatctc aactagaaca atcaaaagag 360
 36 tctctttctt taaataaaac agtgccatca acgtctaat gggagatttg tgattttatt 420
 37 actaaggggg atacccttgt tgggtctttc aaatcagggt ttgaaaagtt atctcaaact 480
 38 gatcatctcg tattgcctag tcaagcagca gatggaactc aattgatata agtagctagt 540
 39 tttgctttta ctccagataa aaagacggca attgcagaat ataccagtag ggctggagaa 600
 40 aatggggaaa taagccaact agatgtggat ggaaaagaaa ttattaacga aggtgagggt 660
 41 tttaattctt atctactaaa gaaggtaaca atcccaactg gttataaaca tattggtcaa 720
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 44 aaagcgattg gagaattagc tttttttgat aatcaaatta caggtaaact ttctttgcc 900
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63 acygcacata attcctacgc actagcagat ggtgagcatt ttatcgttga tccagataag 2040
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78 caatcaaacc caaaaacgaa tagaggacga cactctgcaa tattgcctag gacaggggtca 2940
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80 actgctataa aaaagaaaaa atatttaa 3027

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83 <210> SEQ ID NO: 2

84 <211> LENGTH: 1008

85 <212> TYPE: PRT

86 <213> ORGANISM: Streptococcus pyogenes

88 <400> SEQUENCE: 2

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90 1 5 10 15
92 Val Val Thr His Asn Gln Glu Val Phe Ser Leu Val Lys Glu Pro Ile
93 20 25 30
95 Leu Lys Gln Thr Gln Ala Ser Ser Ser Ile Ser Gly Ala Asp Tyr Ala
96 35 40 45
98 Glu Ser Ser Gly Lys Ser Lys Leu Lys Ile Asn Glu Thr Ser Gly Pro
99 50 55 60
101 Val Asp Asp Thr Val Thr Asp Leu Phe Ser Asp Lys Arg Thr Thr Pro
102 65 70 75 80
104 Glu Lys Ile Lys Asp Asn Leu Ala Lys Gly Pro Arg Glu Gln Glu Leu
105 85 90 95
107 Lys Ala Val Thr Glu Asn Thr Glu Ser Glu Lys Gln Ile Thr Ser Gly
108 100 105 110
110 Ser Gln Leu Glu Gln Ser Lys Glu Ser Leu Ser Leu Asn Lys Thr Val
111 115 120 125
113 Pro Ser Thr Ser Asn Trp Glu Ile Cys Asp Phe Ile Thr Lys Gly Asn

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114	130	135	140
116	Thr Leu Val Gly Leu Ser Lys Ser Gly Val Glu Lys Leu Ser Gln Thr		
117	145	150	155
119	Asp His Leu Val Leu Pro Ser Gln Ala Ala Asp Gly Thr Gln Leu Ile		
120		165	170
122	Gln Val Ala Ser Phe Ala Phe Thr Pro Asp Lys Lys Thr Ala Ile Ala		
123		180	185
125	Glu Tyr Thr Ser Arg Ala Gly Glu Asn Gly Glu Ile Ser Gln Leu Asp		
126		195	200
128	Val Asp Gly Lys Glu Ile Ile Asn Glu Gly Glu Val Phe Asn Ser Tyr		
129	210	215	220
131	Leu Leu Lys Lys Val Thr Ile Pro Thr Gly Tyr Lys His Ile Gly Gln		
132	225	230	235
134	Asp Ala Phe Val Asp Asn Lys Asn Ile Ala Glu Val Asn Leu Pro Glu		
135		245	250
137	Ser Leu Glu Thr Ile Ser Asp Tyr Ala Phe Ala His Leu Ala Leu Lys		
138		260	265
140	Gln Ile Asp Leu Pro Asp Asn Leu Lys Ala Ile Gly Glu Leu Ala Phe		
141		275	280
143	Phe Asp Asn Gln Ile Thr Gly Lys Leu Ser Leu Pro Arg Gln Leu Met		
144	290	295	300
146	Arg Leu Ala Glu Arg Ala Phe Lys Ser Asn His Ile Lys Thr Ile Glu		
147	305	310	315
149	Phe Arg Gly Asn Ser Leu Lys Val Ile Gly Glu Ala Ser Phe Gln Asp		
150		325	330
152	Asn Asp Leu Ser Gln Leu Met Leu Pro Asp Gly Leu Glu Lys Ile Glu		
153		340	345
155	Ser Glu Ala Phe Thr Gly Asn Pro Gly Asp Asp His Tyr Asn Asn Arg		
156		355	360
158	Val Val Leu Trp Thr Lys Ser Gly Lys Asn Pro Ser Gly Leu Ala Thr		
159	370	375	380
161	Glu Asn Thr Tyr Val Asn Pro Asp Lys Ser Leu Trp Gln Glu Ser Pro		
162	385	390	395
164	Glu Ile Asp Tyr Thr Lys Trp Leu Glu Glu Asp Phe Thr Tyr Gln Lys		
165		405	410
167	Asn Ser Val Thr Gly Phe Ser Asn Lys Gly Leu Gln Lys Val Lys Arg		
168		420	425
170	Asn Lys Asn Leu Glu Ile Pro Lys Gln His Asn Gly Val Thr Ile Thr		
171		435	440
173	Glu Ile Gly Asp Asn Ala Phe Arg Asn Val Asp Phe Gln Asn Lys Thr		
174	450	455	460
176	Leu Arg Lys Tyr Asp Leu Glu Glu Val Lys Leu Pro Ser Thr Ile Arg		
177	465	470	475
179	Lys Ile Gly Ala Phe Ala Phe Gln Ser Asn Asn Leu Lys Ser Phe Glu		
180		485	490
182	Ala Ser Asp Asp Leu Glu Glu Ile Lys Glu Gly Ala Phe Met Asn Asn		
183		500	505
185	Arg Ile Glu Thr Leu Glu Leu Lys Asp Lys Leu Val Thr Ile Gly Asp		
186	515	520	525

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188 Ala Ala Phe His Ile Asn His Ile Tyr Ala Ile Val Leu Pro Glu Ser
189      530      535      540
191 Val Gln Glu Ile Gly Arg Ser Ala Phe Arg Gln Asn Gly Ala Asn Asn
192 545      550      555      560
194 Leu Ile Phe Met Gly Ser Lys Val Lys Thr Leu Gly Glu Met Ala Phe
195      565      570      575
197 Leu Ser Asn Arg Leu Glu His Leu Asp Leu Ser Glu Gln Lys Gln Leu
198      580      585      590
200 Thr Glu Ile Pro Val Gln Ala Phe Ser Asp Asn Ala Leu Lys Glu Val
201      595      600      605
203 Leu Leu Pro Ala Ser Leu Lys Thr Ile Arg Glu Glu Ala Phe Lys Lys
204      610      615      620
206 Asn His Leu Lys Gln Leu Glu Val Ala Ser Ala Leu Ser His Ile Ala
207 625      630      635      640
209 Phe Asn Ala Leu Asp Asp Asn Asp Gly Asp Glu Gln Phe Asp Asn Lys
210      645      650      655
212 Val Val Val Lys Thr His His Asn Ser Tyr Ala Leu Ala Asp Gly Glu
213      660      665      670
215 His Phe Ile Val Asp Pro Asp Lys Leu Ser Ser Thr Ile Val Asp Leu
216      675      680      685
218 Glu Lys Ile Leu Lys Leu Ile Glu Gly Leu Asp Tyr Ser Thr Leu Arg
219      690      695      700
221 Gln Thr Thr Gln Thr Gln Phe Arg Asp Met Thr Thr Ala Gly Lys Ala
222 705      710      715      720
224 Leu Leu Ser Lys Ser Asn Leu Arg Gln Gly Glu Lys Gln Lys Phe Leu
225      725      730      735
227 Gln Glu Ala Gln Phe Phe Leu Gly Arg Val Asp Leu Asp Lys Ala Ile
228      740      745      750
230 Ala Lys Ala Glu Lys Ala Leu Val Thr Lys Lys Ala Thr Lys Asn Gly
231      755      760      765
233 Gln Leu Leu Glu Arg Ser Ile Asn Lys Ala Val Leu Ala Tyr Asn Asn
234      770      775      780
236 Ser Ala Ile Lys Lys Ala Asn Val Lys Arg Leu Glu Lys Glu Leu Asp
237 785      790      795      800
239 Leu Leu Thr Gly Leu Val Glu Gly Lys Gly Pro Leu Ala Gln Ala Thr
240      805      810      815
242 Met Val Gln Gly Val Tyr Leu Leu Lys Thr Pro Leu Pro Leu Pro Glu
243      820      825      830
245 Tyr Tyr Ile Gly Leu Asn Val Tyr Phe Asp Lys Ser Gly Lys Leu Ile
246      835      840      845
248 Tyr Ala Leu Asp Met Ser Asp Thr Ile Gly Glu Gly Gln Lys Asp Ala
249      850      855      860
251 Tyr Gly Asn Pro Ile Leu Asn Val Asp Glu Asp Asn Glu Gly Tyr His
252 865      870      875      880
254 Ala Leu Ala Val Ala Thr Leu Ala Asp Tyr Glu Gly Leu Asp Ile Lys
255      885      890      895
257 Thr Ile Leu Asn Ser Lys Leu Ser Gln Leu Thr Ser Ile Arg Gln Val
258      900      905      910
260 Pro Thr Ala Ala Tyr His Arg Ala Gly Ile Phe Gln Ala Ile Gln Asn

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261          915          920          925
263 Ala Ala Ala Glu Ala Glu Gln Leu Leu Pro Lys Pro Gly Thr His Ser
264          930          935          940
266 Glu Lys Ser Ser Ser Ser Glu Ser Ala Asn Ser Lys Asp Arg Gly Leu
267 945          950          955          960
269 Gln Ser Asn Pro Lys Thr Asn Arg Gly Arg His Ser Ala Ile Leu Pro
270          965          970          975
272 Arg Thr Gly Ser Lys Gly Ser Phe Val Tyr Gly Ile Leu Gly Tyr Thr
273          980          985          990
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276          995          1000          1005
279 <210> SEQ ID NO: 3
280 <211> LENGTH: 951
281 <212> TYPE: PRT
282 <213> ORGANISM: Streptococcus pyogenes
284 <400> SEQUENCE: 3
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289          20          25          30
291 Thr Thr Pro Glu Lys Ile Lys Asp Asn Leu Ala Lys Gly Pro Arg Glu
292          35          40          45
294 Gln Glu Leu Lys Ala Val Thr Glu Asn Thr Glu Ser Glu Lys Gln Ile
295 50          55          60
297 Thr Ser Gly Ser Gln Leu Glu Gln Ser Lys Glu Ser Leu Ser Leu Asn
298 65          70          75          80
300 Lys Arg Val Pro Ser Thr Ser Asn Trp Glu Ile Cys Asp Phe Ile Thr
301          85          90          95
303 Lys Gly Asn Thr Leu Val Gly Leu Ser Lys Ser Gly Val Glu Lys Leu
304          100          105          110
306 Ser Gln Thr Asp His Leu Val Leu Pro Ser Gln Ala Ala Asp Gly Thr
307          115          120          125
309 Gln Leu Ile Gln Val Ala Ser Phe Ala Phe Thr Pro Asp Lys Lys Thr
310          130          135          140
312 Ala Ile Ala Glu Tyr Thr Ser Arg Ala Gly Glu Asn Gly Glu Ile Ser
313 145          150          155          160
315 Gln Leu Asp Val Asp Gly Lys Glu Ile Ile Asn Glu Gly Glu Val Phe
316          165          170          175
318 Asn Ser Tyr Leu Leu Lys Lys Val Thr Ile Pro Thr Gly Tyr Lys His
319          180          185          190
321 Ile Gly Gln Asp Ala Phe Val Asp Asn Lys Asn Ile Ala Glu Val Asn
322          195          200          205
324 Leu Pro Glu Ser Leu Glu Thr Ile Ser Asp Tyr Ala Phe Ala His Leu
325          210          215          220
327 Ala Leu Lys Gln Ile Asp Leu Pro Asp Asn Leu Lys Ala Ile Gly Glu
328 225          230          235          240
330 Leu Ala Phe Phe Asp Asn Gln Ile Thr Gly Lys Leu Ser Leu Pro Arg
331          245          250          255
333 Gln Leu Met Arg Leu Ala Glu Arg Ala Phe Lys Ser Asn His Ile Lys

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/078,531

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Input Set : A:\Pharma18.app
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:14; Xaa Pos. 3,6